



Rec'd PCT/PTO 07 APR 2005
10/509484

SEQUENCE LISTING

<110> Takeda Chemical Industries, Ltd.

<120> Novel Screening Method

<130> P04-117PCT

<150> JP 2002-093045

<151> 2002-03-28

<150> JP 2002-361580

<151> 2002-12-13

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<170> PatentIn version 3.1

<210> 1

<211> 957

<212> DNA

<213> Rattus sp.

<220>

<221> CDS

<222> (1)..(957)

<223> rat-derived rCB7T084

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ccc acc atg gac cct gtg acc tgg gtt tac ttt tca gtg aca ttc ctg	96
Pro Thr Met Asp Pro Val Thr Trp Val Tyr Phe Ser Val Thr Phe Leu	
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gcc atg gcc acc tgt gtg tgt ggg ata gtg ggc aac tcc atg gtg att	144
Ala Met Ala Thr Cys Val Cys Gly Ile Val Gly Asn Ser Met Val Ile	
35 40 45	
tgg cta ctg agt ttc cac agt gtg cag agg tcc ccc ttc tgc acc tac	192
Trp Leu Leu Ser Phe His Ser Val Gln Arg Ser Pro Phe Cys Thr Tyr	
50 55 60	
gtg ctc aac ctg gcg gtg gcc gac ctc ctc ttc ctg ctc tgc atg gcc	240
Val Leu Asn Leu Ala Val Ala Asp Leu Leu Phe Leu Leu Cys Met Ala	
65 70 75 80	
tcc ctg ctc agt ctg gaa aca ggg ccc ctg ctc aca gcc agc acc tcc	288
Ser Leu Leu Ser Leu Glu Thr Gly Pro Leu Leu Thr Ala Ser Thr Ser	
85 90 95	
gcc aga gtc tac gag ggg atg aag aga atc aag tac ttt gcc tac aca	336
Ala Arg Val Tyr Glu Gly Met Lys Arg Ile Lys Tyr Phe Ala Tyr Thr	
100 105 110	
gca ggc ctg agc ctg ctg acg gcc atc agc acc cag cgc tgt ctc tcc	384
Ala Gly Leu Ser Leu Leu Thr Ala Ile Ser Thr Gln Arg Cys Leu Ser	
115 120 125	
gtg ctt ttc ccc atc tgg tat aag tgc cac cgg ccc cag cac ctg tcg	432
Val Leu Phe Pro Ile Trp Tyr Lys Cys His Arg Pro Gln His Leu Ser	
130 135 140	
ggg gtg gta tgt ggt gtg ctg tgg gca ctg gcc ctc ctg atg aac ttc	480

Gly	Val	Val	Cys	Gly	Val	Leu	Trp	Ala	Leu	Ala	Leu	Leu	Met	Asn	Phe		
145					150					155					160		
ctg	gct	tct	ttc	ttc	tgt	gtt	caa	ttc	tgg	cat	ccc	gac	aaa	tac	cag	528	
Leu	Ala	Ser	Phe	Phe	Cys	Val	Gln	Phe	Trp	His	Pro	Asp	Lys	Tyr	Gln		
				165					170						175		
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Cys	Phe	Lys	Val	Asp	Met	Val	Phe	Asn	Ser	Leu	Ile	Leu	Gly	Ile	Phe		
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Lys	Asn	Ser	Leu	Leu	Gln	Arg	Arg	Gln	Pro	Arg	Arg	Leu	Tyr	Val	Val		
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Ile	Leu	Thr	Ser	Val	Leu	Val	Phe	Leu	Thr	Cys	Ser	Leu	Pro	Leu	Gly		
	225				230					235					240		
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Ile	Asn	Trp	Phe	Leu	Leu	Tyr	Trp	Val	Glu	Leu	Pro	Gln	Ala	Val	Arg		
				245					250					255			
ctc	ctg	tac	gtc	tgc	tca	tca	cgc	ttc	tcc	tcg	tct	ttg	agc	agc	agc	816	
Leu	Leu	Tyr	Val	Cys	Ser	Ser	Arg	Phe	Ser	Ser	Ser	Leu	Ser	Ser	Ser		
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gcc	aac	cca	gtc	atc	tac	ttc	ctc	gtg	ggc	agc	cag	aag	agc	cac	cgg	864	
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Leu	Gln	Glu	Ser	Leu	Gly	Ala	Val	Leu	Gly	Arg	Ala	Leu	Gln	Asp	Glu		
	290					295				300							
cct	gaa	ggc	agg	gag	acg	cca	tcc	aca	tgt	act	aat	gat	ggg	gtc		957	
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Ala	Met	Ala	Thr	Cys	Val	Cys	Gly	Ile	Val	Gly	Asn	Ser	Met	Val	Ile		
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Trp	Leu	Leu	Ser	Phe	His	Ser	Val	Gln	Arg	Ser	Pro	Phe	Cys	Thr	Tyr		
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Leu	Ala	Ser	Phe	Phe	Cys	Val	Gln	Phe	Trp	His	Pro	Asp	Lys	Tyr	Gln
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Cys	Phe	Lys	Val	Asp	Met	Val	Phe	Asn	Ser	Leu	Ile	Leu	Gly	Ile	Phe
			180					185					190		
Met	Pro	Val	Met	Val	Leu	Thr	Ser	Ala	Ile	Ile	Phe	Ile	Arg	Met	Arg
		195					200					205			
Lys	Asn	Ser	Leu	Leu	Gln	Arg	Arg	Gln	Pro	Arg	Arg	Leu	Tyr	Val	Val
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Ile	Leu	Thr	Ser	Val	Leu	Val	Phe	Leu	Thr	Cys	Ser	Leu	Pro	Leu	Gly
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Ile	Asn	Trp	Phe	Leu	Leu	Tyr	Trp	Val	Glu	Leu	Pro	Gln	Ala	Val	Arg
			245						250					255	
Leu	Leu	Tyr	Val	Cys	Ser	Ser	Arg	Phe	Ser	Ser	Ser	Leu	Ser	Ser	Ser
			260					265					270		
Ala	Asn	Pro	Val	Ile	Tyr	Phe	Leu	Val	Gly	Ser	Gln	Lys	Ser	His	Arg
		275					280					285			
Leu	Gln	Glu	Ser	Leu	Gly	Ala	Val	Leu	Gly	Arg	Ala	Leu	Gln	Asp	Glu
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tat tcc aga ggg agc aca gtg cac acg gcc tac ctg gtg ctg agc tcc		96
Tyr Ser Arg Gly Ser Thr Val His Thr Ala Tyr Leu Val Leu Ser Ser		
20 25 30		
ctg gcc atg ttc acc tgc ctg tgc ggg atg gca ggc aac agc atg gtg		144
Leu Ala Met Phe Thr Cys Leu Cys Gly Met Ala Gly Asn Ser Met Val		
35 40 45		
atc tgg ctg ctg ggc ttt cga atg cac agg aac ccc ttc tgc atc tat		192
Ile Trp Leu Leu Gly Phe Arg Met His Arg Asn Pro Phe Cys Ile Tyr		
50 55 60		
atc ctc aac ctg gcg gca gcc gac ctc ctc ttc ctc ttc agc atg gct		240
Ile Leu Asn Leu Ala Ala Ala Asp Leu Leu Phe Leu Phe Ser Met Ala		
65 70 75 80		
tcc acg ctc agc ctg gaa acc cag ccc ctg gtc aat acc act gac aag		288
Ser Thr Leu Ser Leu Glu Thr Gln Pro Leu Val Asn Thr Thr Asp Lys		
85 90 95		
gtc cac gag ctg atg aag aga ctg atg tac ttt gcc tac aca gtg ggc		336
Val His Glu Leu Met Lys Arg Leu Met Tyr Phe Ala Tyr Thr Val Gly		
100 105 110		
ctg agc ctg ctg acg gcc atc agc acc cag cgc tgt ctc tct gtc ctc		384
Leu Ser Leu Leu Thr Ala Ile Ser Thr Gln Arg Cys Leu Ser Val Leu		

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ttc cct atc tgg ttc aag tgt cac cgg ccc agg cac ctg tca gcc tgg			432
Phe Pro Ile Trp Phe Lys Cys His Arg Pro Arg His Leu Ser Ala Trp			
130	135	140	
gtg tgt ggc ctg ctg tgg acg ctc tgt ctc ctg atg aac ggg ttg acc			480
Val Cys Gly Leu Leu Trp Thr Leu Cys Leu Leu Met Asn Gly Leu Thr			
145	150	155	160
tct tcc ttc tgc agc aag ttc ttg aaa ttc aat gaa gat cgg tgc ttc			528
Ser Ser Phe Cys Ser Lys Phe Leu Lys Phe Asn Glu Asp Arg Cys Phe			
165	170	175	
agg gtg gac atg gtc cag gcc gcc ctc atc atg ggg gtc tta acc cca			576
Arg Val Asp Met Val Gln Ala Ala Leu Ile Met Gly Val Leu Thr Pro			
180	185	190	
gtg atg act ctg tcc agc ctg acc ctc ttt gtc tgg gtg cgg agg agc			624
Val Met Thr Leu Ser Ser Leu Thr Leu Phe Val Trp Val Arg Arg Ser			
195	200	205	
tcc cag cag tgg cgg cgg cag ccc aca cgg ctg ttc gtg gtg gtc ctg			672
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225	230	235	240
tgg ttt gtg ctc tac tgg ttg agc ctg ccg ccc gag atg cag gtc ctg			768
Trp Phe Val Leu Tyr Trp Leu Ser Leu Pro Pro Glu Met Gln Val Leu			
245	250	255	
tgc ttc agc ttg tca cgc ctc tcc tcg tcc gta agc agc agc gcc aac			816
Cys Phe Ser Leu Ser Arg Leu Ser Ser Ser Val Ser Ser Ser Ala Asn			
260	265	270	
ccc gtc atc tac ttc ctg gtg ggc agc cgg agg agc cac agg ctg ccc			864
Pro Val Ile Tyr Phe Leu Val Gly Ser Arg Arg Ser His Arg Leu Pro			
275	280	285	
acc agg tcc ctg ggg act gtg ctc caa cag gcg ctt cgc gag gag ccc			912
Thr Arg Ser Leu Gly Thr Val Leu Gln Gln Ala Leu Arg Glu Glu Pro			
290	295	300	
gag ctg gaa ggt ggg gag acg ccc acc gtg ggc acc aat gag atg ggg			960
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305	310	315	320
gct			963
Ala			

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 35 40 45
 Ile Trp Leu Leu Gly Phe Arg Met His Arg Asn Pro Phe Cys Ile Tyr
 50 55 60
 Ile Leu Asn Leu Ala Ala Ala Asp Leu Leu Phe Leu Phe Ser Met Ala
 65 70 75 80
 Ser Thr Leu Ser Leu Glu Thr Gln Pro Leu Val Asn Thr Thr Asp Lys

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Val	His	Glu	Leu	Met	Lys	Arg	Leu	Met	Tyr	Phe	Ala	Tyr	Thr	Val	Gly				
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Leu	Ser	Leu	Leu	Thr	Ala	Ile	Ser	Thr	Gln	Arg	Cys	Leu	Ser	Val	Leu				
		115					120						125						
Phe	Pro	Ile	Trp	Phe	Lys	Cys	His	Arg	Pro	Arg	His	Leu	Ser	Ala	Trp				
	130					135					140								
Val	Cys	Gly	Leu	Leu	Trp	Thr	Leu	Cys	Leu	Leu	Met	Asn	Gly	Leu	Thr				
145					150					155					160				
Ser	Ser	Phe	Cys	Ser	Lys	Phe	Leu	Lys	Phe	Asn	Glu	Asp	Arg	Cys	Phe				
				165					170					175					
Arg	Val	Asp	Met	Val	Gln	Ala	Ala	Leu	Ile	Met	Gly	Val	Leu	Thr	Pro				
			180					185					190						
Val	Met	Thr	Leu	Ser	Ser	Leu	Thr	Leu	Phe	Val	Trp	Val	Arg	Arg	Ser				
		195					200					205							
Ser	Gln	Gln	Trp	Arg	Arg	Gln	Pro	Thr	Arg	Leu	Phe	Val	Val	Val	Leu				
	210					215					220								
Ala	Ser	Val	Leu	Val	Phe	Leu	Ile	Cys	Ser	Leu	Pro	Leu	Ser	Ile	Tyr				
225					230					235					240				
Trp	Phe	Val	Leu	Tyr	Trp	Leu	Ser	Leu	Pro	Pro	Glu	Met	Gln	Val	Leu				
			245						250					255					
Cys	Phe	Ser	Leu	Ser	Arg	Leu	Ser	Ser	Val	Ser	Ser	Ser	Ser	Ala	Asn				
		260						265					270						
Pro	Val	Ile	Tyr	Phe	Leu	Val	Gly	Ser	Arg	Arg	Ser	His	Arg	Leu	Pro				
		275					280					285							
Thr	Arg	Ser	Leu	Gly	Thr	Val	Leu	Gln	Gln	Ala	Leu	Arg	Glu	Glu	Pro				
	290					295					300								
Glu	Leu	Glu	Gly	Gly	Glu	Thr	Pro	Thr	Val	Gly	Thr	Asn	Glu	Met	Gly				
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 <212> DNA
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<223> Probe, labeled 5'-terminal with FAM and 3'-terminal with TAMRA

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<223> Primer

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